PCR Amplification and Characterization of Integron-Associated Antimicrobial Resistance Genes from Various Strains of *Salmonella*

Ribot E, Angulo F, Barrett T

Multidrug-resistant *Salmonella* Typhimurium definitive type 104 (DT104) has emerged as the second most commonly isolated strain of *Salmonella* from humans in the United States; approximately 10% of *Salmonella* isolates tested at the Centers for Disease Control and Prevention (CDC) are a similar clone of multidrug-resistant S. Typhimurium DT104. The most common resistance type (R-type) associated with multidrug-resistant *Salmonella* Typhimurium DT104 is ampicillin, chloramphenicol, streptomycin, sulfonamides, and tetracycline (ACSSuT). Antimicrobial resistance in S. Typhimurium DT104 is chromosomally encoded, possibly on an integron, as opposed to plasmid mediated. Integrons are a type of genetic element that allow the integration of cassettes of genetic material, usually antimicrobial resistance genes, into a specific insertion site within the integron. Integrons have been found in both plasmids and the chromosome of various bacteria. This study focused on the identification and characterization of antimicrobial resistance genes associated with integrons found in the chromosome of various strains of *Salmonella*. We have used integron specific oligonucleotides primers to PCR amplify and characterize DNA fragments, from two isolates of *Salmonella* Typhimurium DT104 and six isolates of *Salmonella* of other serotypes (one Java, three Newport, one Ohio, and one Paratyphi a). Nucleotide sequence analysis shows that all strains contain genes implicated in resistance to antimicrobials, but not all the strains contain the same genes within the identified integron. While all the *Salmonella* Typhimurium DT104 yielded PCR products of the same size, some strains belonging to different serotypes yielded PCR products of different sizes. The variation in the genetic content and order of genes within the integron among different strains of *Salmonella* suggest integrons could be used as a possible tool for subtyping. In addition, by studying the genetic arrangement of integron-associated genes, one could possibly attempt to establish evolutionary relationships between different isolates. Finally, the fact that integrons appear to be widely spread among bacteria (in plasmids and in the chromosome) suggest that these antimicrobial genes can be passed both vertically and horizontally between different strains.

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